

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel Use of EDG Receptor

<130> 3127W00P

<150> JP 2002-361415

<151> 2002-12-12

<160> 45

<210> 1

<211> 364

<212> PRT

<213> human

<400> 1

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Met Ala Ala Ile Ser Thr Ser Ile Pro Val Ile Ser Gln Pro Gln Phe
      5              10              15
Thr Ala Met Asn Glu Pro Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
      20              25              30
Phe Tyr Asn Arg Ser Gly Lys His Leu Ala Thr Glu Trp Asn Thr Val
      35              40              45
Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Ile Phe Ile Met
      50              55              60
Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
      65              70              75              80
His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe
      85              90              95
Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn
      100             105             110
Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile
      115             120             125
Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile
      130             135             140

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Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser
 145 150 155 160
 Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile
 165 170 175
 Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile
 180 185 190
 Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val
 195 200 205
 Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu
 210 215 220
 Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser
 225 230 235 240
 Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu
 245 250 255
 Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr
 260 265 270
 Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp
 275 280 285
 Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser
 290 295 300
 Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala
 305 310 315 320
 Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly
 325 330 335
 Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile
 340 345 350
 Leu Ala Gly Val His Ser Asn Asp His Ser Val Val
 355 360

<210> 2

<211> 1092

<212> DNA

<213> human

<400> 2

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cttgccacag aatggaacac agtcagcaag ctggtgatgg gacttggaat cactgtttgt 180
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cattttccta tttattacct aatggctaata ctggctgctg cagacttctt tgctgggttg 300
gcctacttct atctcatgtt caacacagga cccaatactc ggagactgac tgtagcaca 360
tggtcctgc gtcagggcct cattgacacc agcctgacgg catctgtggc caacttactg 420
gctattgcaa tcgagaggca cattacgggtt ttccgcatgc agtccacac acggatgagc 480
aaccggcggg tagtggtggt cattgtgggtc atctggacta tggccatcgt tatgggtgct 540
ataccacagtg tgggctggaa ctgtatctgt gatattgaaa attgttccaa catggcaccc 600
ctctacagtg actcttactt agtcttctgg gccattttca acttggtgac ctttgtggtg 660
atggtggttc tctatgtcca catctttggc tatgttcgcc agaggactat gagaatgtct 720
cggcatagtt ctggaccccg gcggaatcgg gataccatga tgagtcttct gaagactgtg 780
gtcattgtgc ttggggcctt tatcatctgc tggactcctg gattggtttt gttacttcta 840
gacgtgtgct gtccacagtg cgacgtgctg gcctatgaga aattcttctt tctccttgct 900
gaattcaact ctgcatgaa ccccatcatt tactcctacc gcgacaaaga aatgagcgcc 960
acctttaggc agatcctctg ctgccagcgc agtgagaacc ccaccggccc cacagaaggc 1020
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<210> 3

<211> 364

<212> PRT

<213> Rat

<400> 3

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Met Ala Ala Ala Ser Thr Ser Ser Pro Val Ile Ser Gln Pro Gln Phe
      5              10              15
Thr Ala Met Asn Glu Gln Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
      20              25              30
Phe Tyr Asn Arg Ser Gly Lys Tyr Leu Ala Thr Glu Trp Asn Thr Val
      35              40              45
Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Val Phe Ile Met
      50              55              60
Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
      65              70              75              80
His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe
      85              90              95
Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn

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100	105	110	
Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile			
115	120	125	
Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile			
130	135	140	
Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser			
145	150	155	160
Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile			
165	170	175	
Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile			
180	185	190	
Asp His Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val			
195	200	205	
Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu			
210	215	220	
Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser			
225	230	235	240
Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu			
245	250	255	
Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Val Cys Trp Thr			
260	265	270	
Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp			
275	280	285	
Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser			
290	295	300	
Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala			
305	310	315	320
Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Asn Glu Asn Pro Asn Gly			
325	330	335	
Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile			
340	345	350	
Leu Ala Gly Val His Ser Asn Asp His Ser Val Val			
355	360		

<210> 4

<211> 1092

<212> DNA

<213> Rat

<400> 4

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ctagccacag aatggaacac tgtgagcaag ctggtgatgg gactgggcat cactgtctgc   180
gtgttcacaa tgctggccaa tctactggtc atggtggcaa ttacgtcaa ccgccgttc   240
catttccta tttattactt gatggccaac ctggctgctg cagacttctt cgctggactg   300
gcctacttct acctgatgtt caacacggga cctaataccc ggagactgac cgtgagcaca   360
tggtcttccc ggcagggcct catcgacacc agcctgacgg cttctgtggc caacctgctg   420
gccattgcca tcgagaggca catcacagtt ttccgaatgc agtccatac acgaatgagc   480
aaccgacgtg tgggtggtgt gattgtagtc atctggacta tggccattgt gatgggtgcc   540
ataccacgtg tgggctggaa ctgcatctgt gatatcgatc attgttcaa catggcgccc   600
ctctacagtg actcctactt agtcttctgg gccattttca acctgggtgac ctttgtggtc   660
atggtggttc tctacgtca catctttggc tatgttcgcc agaggactat gagaatgtcc   720
cggcatagtt ctggaccag gaggaatcgg gacaccatga tgagccttct gaagactgtg   780
gtcattgtgc tgggtgcctt tattgtctgc tggactccgg gattggtctt gctactgctc   840
gatgtgtgtt gccgcagtg cgaatgctgt gcctatgaga agttcttctt cctcctggcc   900
gagttcaact ctgctatgaa ccccatcacc tactcctacc gcgacaaaga gatgagcgcc   960
accttcaggc agatcctgtg ttgccagcgc aacgagaacc ccaacggccc cacggaaggc  1020
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<210> 5

<211> 378

<212> PRT

<213> human

<400> 5

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Met Ala Thr Ala Leu Pro Pro Arg Leu Gln Pro Val Arg Gly Asn Glu
      5              10              15
Thr Leu Arg Glu His Tyr Gln Tyr Val Gly Lys Leu Ala Gly Arg Leu
      20              25              30
Lys Glu Ala Ser Glu Gly Ser Thr Leu Thr Thr Val Leu Phe Leu Val
      35              40              45
Ile Cys Ser Phe Ile Val Leu Glu Asn Leu Met Val Leu Ile Ala Ile
      50              55              60

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Trp Lys Asn Asn Lys Phe His Asn Arg Met Tyr Phe Phe Ile Gly Asn
 65 70 75 80
 Leu Ala Leu Cys Asp Leu Leu Ala Gly Ile Ala Tyr Lys Val Asn Ile
 85 90 95
 Leu Met Ser Gly Lys Lys Thr Phe Ser Leu Ser Pro Thr Val Trp Phe
 100 105 110
 Leu Arg Glu Gly Ser Met Phe Val Ala Leu Gly Ala Ser Thr Cys Ser
 115 120 125
 Leu Leu Ala Ile Ala Ile Glu Arg His Leu Thr Met Ile Lys Met Arg
 130 135 140
 Pro Tyr Asp Ala Asn Lys Arg His Arg Val Phe Leu Leu Ile Gly Met
 145 150 155 160
 Cys Trp Leu Ile Ala Phe Thr Leu Gly Ala Leu Pro Ile Leu Gly Trp
 165 170 175
 Asn Cys Leu His Asn Leu Pro Asp Cys Ser Thr Ile Leu Pro Leu Tyr
 180 185 190
 Ser Lys Lys Tyr Ile Ala Phe Cys Ile Ser Ile Phe Thr Ala Ile Leu
 195 200 205
 Val Thr Ile Val Ile Leu Tyr Ala Arg Ile Tyr Phe Leu Val Lys Ser
 210 215 220
 Ser Ser Arg Lys Val Ala Asn His Asn Asn Ser Glu Arg Ser Met Ala
 225 230 235 240
 Leu Leu Arg Thr Val Val Ile Val Val Ser Val Phe Ile Ala Cys Trp
 245 250 255
 Ser Pro Leu Phe Ile Leu Phe Leu Ile Asp Val Ala Cys Arg Val Gln
 260 265 270
 Ala Cys Pro Ile Leu Phe Lys Ala Gln Trp Phe Ile Val Leu Ala Val
 275 280 285
 Leu Asn Ser Ala Met Asn Pro Val Ile Tyr Thr Leu Ala Ser Lys Glu
 290 295 300
 Met Arg Arg Ala Phe Phe Arg Leu Val Cys Asn Cys Leu Val Arg Gly
 305 310 315 320
 Arg Gly Ala Arg Ala Ser Pro Ile Gln Pro Ala Leu Asp Pro Ser Arg
 325 330 335
 Ser Lys Ser Ser Ser Ser Asn Asn Ser Ser His Ser Pro Lys Val Lys
 340 345 350
 Glu Asp Leu Pro His Thr Asp Pro Ser Ser Cys Ile Met Asp Lys Asn

355 360 365
 Ala Ala Leu Gln Asn Gly Ile Phe Cys Asn
 370 375

<210> 6
 <211> 1134
 <212> DNA
 <213> human

<400> 6
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 ctcaccaccg tgctcttctt ggtcatctgc agcttcatcg tcttggagaa cctgatggtt 180
 ttgattgcc a tctggaaaa caataaat t cacaaccgca tgtacttttt cattggcaac 240
 ctggctctct gcgacctgct ggccggcatc gcttacaagg tcaacattct gatgtctggc 300
 aagaagacgt tcagcctgtc tcccacggtc tggttcctca gggagggcag tatgttcgtg 360
 gcccttgggg cgtccacctg cagcttactg gccatcgcca tcgagcggca cttgacaatg 420
 atcaaaatga ggccttacga cgccaacaag aggcaccgcg tcttctctct gatcgggatg 480
 tgctggetca ttgccttcac gctgggcgcc ctgccattc tgggctggaa ctgcctgcac 540
 aatctccctg actgctctac catcctgccc ctctactcca agaagtacat tgccttctgc 600
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 ctggtgaagt ccagcagccg taaggtggcc aaccacaaca actcggagcg gtccatggca 720
 ctgctgcgga ccgtggtgat tgtggtgagc gtgttcatcg cctgctggtc cccactcttc 780
 atctcttcc tcattgatgt ggcctgcagg gtgcaggcgt gccccatcct cttcaaggct 840
 cagtgttca tcgtgttggc tgtgtcaac tccgccatga acccggtcat ctacacgctg 900
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 cggggggccc gcgcctcacc catccagcct gcgctcgacc caagcagaag taaatcaagc 1020
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<210> 7
 <211> 222
 <212> PRT
 <213> Rat

<400> 7
 Arg Met Tyr Phe Phe Ile Gly Asn Leu Ala Leu Cys Asp Leu Leu Ala

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Gly Ile Ala Tyr Lys Val Asn Ile Leu Met Ser Gly Arg Lys Thr Phe			
	20	25	30
Ser Leu Ser Pro Thr Val Trp Phe Leu Arg Glu Gly Ser Met Phe Val			
	35	40	45
Ala Leu Gly Ala Ser Thr Cys Ser Leu Leu Ala Ile Ala Ile Glu Arg			
	50	55	60
His Leu Thr Met Ile Lys Met Arg Pro Tyr Asp Ala Asn Lys Lys His			
	65	70	75
Arg Val Phe Leu Leu Ile Gly Met Cys Trp Leu Ile Ala Phe Ser Leu			
	85	90	95
Gly Ala Leu Pro Ile Leu Gly Trp Asn Cys Leu Glu Asn Phe Pro Asp			
	100	105	110
Cys Ser Thr Ile Leu Pro Leu Tyr Ser Lys Lys Tyr Ile Ala Phe Leu			
	115	120	125
Ile Ser Ile Phe Thr Ala Ile Leu Val Thr Ile Val Ile Leu Tyr Ala			
	130	135	140
Arg Ile Tyr Phe Leu Val Lys Ser Ser Ser Arg Arg Val Ala Asn His			
	145	150	155
Asn Ser Glu Arg Ser Met Ala Leu Leu Arg Thr Val Val Ile Val Val			
	165	170	175
Ser Val Phe Ile Ala Cys Trp Ser Pro Leu Phe Ile Leu Phe Leu Ile			
	180	185	190
Asp Val Ala Cys Arg Ala Lys Glu Cys Ser Ile Leu Phe Lys Ser Gln			
	195	200	205
Trp Phe Ile Met Leu Ala Val Leu Asn Ser Ala Met Asn Pro			
	210	215	220

<210> 8

<211> 666

<212> DNA

<213> Rat

<400> 8

cgcatgtact ttttcattgg caacttggct ctctgcgacc tgctggccgg catagcctac	60
aaggtcaaca ttctgatgtc cggttaggaag acgttcagcc tgtctccaac agtgtggttc	120
ctcagggagg gcagtatgtt cgtagccctg ggcgcatcca catgcagctt attggccatt	180


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gccattgagc ggcacctgac catgatcaag atgaggccgt acgacgcaa caagaagcac 240
cgcggtgtcc ttctgattgg gatgtgctgg ctaattgcct tctcgctggg tgccctgccc 300
atcctgggct ggaactgcct ggagaacttt cccgactgct ctaccatctt gcccctctac 360
tccaagaaat acattgcctt tctcatcagc atcttcacag ccattctggt gaccatcgtc 420
atcttgtacg cgcgcatcta cttcctggtc aagtccagca gccgcagggt ggccaaccac 480
aactccgaga gatccatggc ccttctgcgg accgtagtga tcgtggtgag cgtgttcac 540
gcctgttggt cccccctttt catcctcttc ctcacgatg tggcctgcag ggccaaggag 600
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<210> 9

<211> 353

<212> PRT

<213> human

<400> 9

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Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
      5              10              15
His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
      20              25              30
Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
      35              40              45
Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
      50              55              60
His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
      65              70              75              80
Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
      85              90              95
Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
     100             105             110
Ser Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
     115             120             125
Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
     130             135             140
Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
     145             150             155             160
Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu

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10/23

165	170	175
Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu		
180	185	190
Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu		
195	200	205
Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala		
210	215	220
Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly		
225	230	235
Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp		
245	250	255
Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr		
260	265	270
Phe Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr		
275	280	285
Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln		
290	295	300
Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Val Gly Thr		
305	310	315
Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg		
325	330	335
Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val		
340	345	350
Val		

<210> 10

<211> 1059

<212> DNA

<213> human

<400> 10

atgggcagct tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat	60
accaaggaga cgctggaaac gcaggagacg acctcccgcc aggtggcctc ggccttcac	120
gtcatcctct gttgcgcat tgtggtggaa aaccttctgg tgctcattgc ggtggcccga	180
aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta	240
ctggcaggcg tggccttcgt agccaatacc ttgctctctg gctctgtcac gctgaggctg	300
acgcctgtgc agtggtttgc ccgggagggc tctgcctcca tcacgtcttc ggcctctgtc	360

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ttcagcctcc tggccatcgc cattgagcgc cacgtggcca ttgccaaggt caagctgtat 420
ggcagcgaca agagctgccg catgtttctg ctcatcgggg cctcgtggct catctcgctg 480
gtcctcggtg gcctgcccac ccttggcttg aactgcctgg gccacctcga ggccgtgctcc 540
actgtcctgc ctctctacgc caagcattat gtgtgtgtgc tggtgacctt cttctccatc 600
atcctgttgg ccatcgtggc cctgtacgtg cgcacttact gcgtgggtccg ctcaagccac 660
gctgacatgg cgcggccgca gacgctagcc ctgctcaaga cggtcaccat cgtgctaggg 720
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gtccactcct gcccgatcct ctacaaagcc cactactttt tcgccgtctc caccctgaat 840
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cggccgctgc agtgtgtggc gccgggggtg ggggtgcaag gacggaggcg ggtcggggacc 960
ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg 1020
cccacgtcac ccacgtttct ggagggaac acggtggtc 1059

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<210> 11

<211> 352

<212> PRT

<213> Rat

<400> 11

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Met Gly Gly Leu Tyr Ser Glu Tyr Leu Asn Pro Glu Lys Val Gln Glu
      5              10              15
His Tyr Asn Tyr Thr Lys Glu Thr Leu Asp Met Gln Glu Thr Pro Ser
      20              25              30
Arg Lys Val Ala Ser Ala Phe Ile Ile Ile Leu Cys Cys Ala Ile Val
      35              40              45
Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
      50              55              60
His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
      65              70              75              80
Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Pro Val
      85              90              95
Thr Leu Ser Leu Thr Pro Leu Gln Trp Phe Ala Arg Glu Gly Ser Ala
      100             105             110
Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
      115             120             125
Glu Arg Gln Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
      130             135             140

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Ser Cys Arg Met Leu Met Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
 145 150 155 160
 Ile Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Asp His Leu
 165 170 175
 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
 180 185 190
 Cys Val Val Thr Ile Phe Ser Val Ile Leu Leu Ala Ile Val Ala Leu
 195 200 205
 Tyr Val Arg Ile Tyr Phe Val Val Arg Ser Ser His Ala Asp Val Ala
 210 215 220
 Gly Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
 225 230 235 240
 Val Phe Ile Ile Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
 245 250 255
 Ser Thr Cys Pro Val Arg Ala Cys Pro Val Leu Tyr Lys Ala His Tyr
 260 265 270
 Phe Phe Ala Phe Ala Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
 275 280 285
 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Leu
 290 295 300
 Cys Trp Arg Gln Gly Lys Gly Ala Thr Gly Arg Arg Gly Gly Asn Pro
 305 310 315 320
 Gly His Arg Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg Gly
 325 330 335
 Leu His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val Val
 340 345 350

<210> 12

<211> 1056

<212> DNA

<213> Rat

<400> 12

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 atcattttat gctgtgccat cgtgggtggag aaccttctgg tgctaatcgc agtggccagg 180
 aacagcaagt tccactcagc catgtacctg ttccctcgga acctggcagc ctccgacctg 240

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ctggcaggcg tggccttcgt ggccaacacc ttgctctccg gacctgtcac cctgtcctta 300
actcccttgc agtgggttgc ccgagagggt tcagccttca tcacgtcttc tgcctcggtc 360
ttcagcctcc tggccattgc catcgagaga caagtggcca tcgccaaggt caagctctac 420
ggcagtgaca aaagctgtcg aatgttgatg ctcatgggg cctcttggct gatatcgctg 480
attctgggtg gcttgcccat cctgggctgg aattgtctgg accatctgga ggcttgcctc 540
actgtgctgc ccctctatgc taagcactat gtgctctgcg tggtcacat cttctctgtc 600
atcttactgg ctatcgtggc cttgtacgtc cgaatctact tcgtagtccg ctcaagccat 660
gcgagcgttg ctggtcctca gacgttggcc ctgctcaaga cagtcacat cgtactgggt 720
gttttcatca tctgctggct gccggctttt agcatccttc tcttagactc tacctgtccc 780
gtccgggcct gtcctgtcct ctacaaagcc cattatttct ttgccttcgc caccctcaac 840
tctctgtcga accctgtcat ctatacatgg cgtagccggg accttcggag ggaggtactg 900
aggcccctgc tgtgctggcg gcaggggaag ggagcaacag ggcgcagagg tgggaaccct 960
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acatgccaa catttctgga gggcaacaca gtggtc 1056

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<210> 13

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 13

ccaccgaccc atgtactatt tt

22

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 14

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22

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<223> Probe, labeled 5'-terminal with FAM and 3'-terminal with TAMRA

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22

<210> 16

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<220>

<223> Primer

<400> 16

actgtcagca catggctcct t

21

<210> 17

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<212> DNA

<213> Artificial Sequence

<220>

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<400> 17

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21

<210> 18

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<400> 18

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22

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<223> Primer

<400> 19

ccgtgctctt cttggtcat

19

<210> 20

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20

ccagatggca atcaaaacc

19

<210> 21

<211> 26

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26

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<223> Primer

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cctggtaag actgttgta tc

22

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<212> DNA

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<220>

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<400> 23

caggacattg caggactca

19

<210> 24

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27

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<220>

<223> Primer

<400> 25

ccaacaaggt ccaggaaca

19

<210> 26

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

aggttttcca ccacaatgg

19

<210> 27

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28

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gaactgcctg tgcgccttt

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<400> 29

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20

<210> 30

<211> 28

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tgactgcttc cctcaccaa

19

<210> 32

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<400> 32

gcatcctcat gattgacatg tg

22

<210> 33

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22

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<400> 34

cttgctccac tgtcttgcc

19

<210> 35

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tagagtgcac agatcgcg

19

<210> 36

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28

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25

<210> 38

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<213> Artificial Sequence

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<400> 38

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21

<210> 39

<211> 28

<212> DNA

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28

<210> 40

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<223> Primer

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atcttgtacg cgcgcatcta

20

<210> 41

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<223> Primer

<400> 41

tggatctctc ggagttgtgg tt

22

<210> 42

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<400> 42

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22

<210> 43

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gtttgcccga gagggttca

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<210> 44

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<400> 44

cttgtctctc gatggcaatg g

21

<210> 45

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Probe, labeled 5'-terminal with FAM and 3'-terminal with TAMRA

<400> 45

cttcatcacg ctctctgcct cggctctt

27